REMARKS

The specification has been amended to recite the SEQ ID Numbers for the nucleic acid sequence of Genbank Accession No. X69822 and the amino acid sequence encoded thereby.

Claims 1, 2, 7 and 18 have also been amended to obviate the 35 U.S.C. §112, second paragraph rejection set forth in the present Official Action.

All of the foregoing amendments are presented to further clarify the scope of the invention and in no way represent acquiescence to the rejections made by the Examiner.

The April 11, 2003 Official Action and references cited therein have been carefully reviewed. In light of the amendments presented herewith and the following remarks, favorable reconsideration and allowance of the application are respectfully requested.

At the outset, the Examiner indicates at page 7 that claims 12, 16-18, 20-22, 29, and 30 are deemed free of the prior art. Notably, claim 2 has been rejected under 35 U.S.C. §112, second paragraph only. Accordingly, Applicants assume that claim 2 is also free of the prior art.

At page 3 of the Official Action, the Examiner maintains the rejection of claims 17 and 30 under 35 U.S.C. §112, first paragraph as allegedly containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Applicants again reiterate that the INRA clone of claims 17 and 30 is readily available to the public and further that this particular clone is not essential to the practice of the instant invention. Attached hereinwith, please find two references where clone INRa 717 1-B4 was used, Siebrecht et al. *Journal of experimental Botany* 1999;50(341):1797-1806 and Lapierre et al. *Plant Physiology* 1999;119:153-163. However,

in order to advance prosecution, these claims are cancelled in accordance with the present amendment.

At page 3, the Examiner indicates that claims 2, 7-12, 16-18, 20-22, and 29-30 remain rejected under 35 U.S.C. §112, second paragraph, for the reasons set forth in the Official Action of July 8, 2002. However, it is noted that the Examiner has stated that the previous rejection of claims 7, 12-27, 31, and 40 under 35 U.S.C. §112, second paragraph, has been withdrawn in view of Applicant's amendments. While the current Official Action provides a basis for the rejection of claims 2, 7, 11, 12, 18, 19, and 21 under 35 U.S.C. §112, second paragraph, the Action is silent regarding the grounds for the assertion that claims 8, 9, 10, 16, 17, 20, 22, 29, and 30 are lacking in clarity. Clarification is respectfully requested.

The Examiner has rejected claims 1 and 7 under 35 U.S.C. §102(e) as allegedly being anticipated by US Patent 5,955,651 to Corruzzi et al.

Claims 1 and 7-11 are rejected under 35 U.S.C. §103(a) as allegedly unpatentable over Coruzzi et al. (U.S. Patent No. 5,955,651) in view of Canton F. et al. (Plant Molecular Biology, 1993, Vol. 22, pp.819-822) and Applicant's admission.

The foregoing constitutes the entirety of the objections and rejections raised in the April 11, 2003 Official Action. In light of the present amendments and the following remarks, each of the above-noted rejections under 35 U.S.C. §§ 112, first and second paragraphs, 102(e), and 103(a) is respectfully traversed.

SEQUENCE LISTING

A paper copy of the amended sequence listing in compliance with 37 C.F.R. §§1.821-1.825 is being submitted herewith providing sequence information for the nucleic acid sequence of Genbank Accession No. X69822 and the amino acid

sequence of the protein encoded thereby. Both the nucleic acid and amino acid sequences were provided when the skilled person accessed GenBank Accession number X69822 at the time the application was filed. Accordingly, Applicants submit that the provision of the nucleic acid and amino acid sequences in the attached sequence listing does not introduce new matter into the application. This statement provides the requisite evidence to support entry of the sequence into the application (see MPEP 608.01(p), which discusses the incorporation of essential material into the specification).

The sequence listing is being submitted in both paper copy and computer readable form under a separate cover in order to facilitate entry of the same into the application. Entry of the sequence listing is respectfully requested.

CLAIMS 2, 7, 11, 12, 18, AND 21 AS AMENDED FULLY COMPLY WITH THE DEFINITIVENESS REQUIREMENT OF U.S.C. §112, SECOND PARAGRAPH

It is the Examiner's position that the phrase "Genbank Accession No. X69822" renders claims 2 and 7 indefinite. Applicants disagree with the Examiner's assertion. However, in order to expedite prosecution, claims 2 and 7 have been amended to replace the phrase "Genbank Accession No. X69822" with "SEQ ID NO: 3". The cancellation of the b) clause from claim 7 renders the Examiner's rejection of this claim moot. The substitute sequence listing submitted herewith designates the nucleic acid provided in Genbank Accession No. X69822, as SEQ ID NO: 3. The amino acid sequence encoded thereby is designated as SEQ ID NO: 4. It is respectfully requested that the amendments to the specification inserting these sequence identifiers where appropriate be entered in the above-identified application.

The Examiner further rejects claim 7 asserting that the phrase "encodes a protein having enzymatic function" renders

the metes and bounds of the claim unclear. Claim 7 has been amended to recite that the sequence "encodes a protein having glutamate synthetase activity", which is clear and definite.

Applicants have also followed the Examiner's helpful suggestion made the following claim amendments: 1) The "the" has been replaced with an "a" in claim 11; 2) "said plant" has been replaced with "a plant" in claim 12; and 3) claim 18 has been amended to recite "wherein the transforming is by *Agrobacterium tumefaciens* mediated transformation".

The Examiner also asserts that claim 19 is improperly dependent. Inasmuch as claim 19 was canceled in the previous response, this rejection of claim 19 is moot.

Additionally, the Examiner maintains the rejection of claim 21 asserting that the phrase "a reproductive unit" is indefinite. Applicants hereby reiterate the position that "a reproductive unit" is clear and definite to those skilled in the art of plant biology. See U.S. Patent Nos. 5,861,542 and 6,194,167. In the '542 patent, a "reproductive unit" of a plant was defined as "any totipotent part or tissue of the plant from which one can obtain a progeny of the plant, including, for example, seeds, cuttings, buds, bulbs, somatic embryos, etc." In the '167 patent, the term "a reproductive unit" of a plant was similarly defined as "any totipotent part or tissue of the plant from which one can obtain a progeny of the plant, including, for example, seeds, cuttings, tubers, buds, bulbs, somatic embryos, cultured cells (e.g., callus or suspension cultures), etc." It is a well settled premise in patent law that "a patent need not teach, and preferably omits, what is well known in the art." Lindemann Maschinenfabrik v. American Hoist and Derrick, 221 USPQ 481, 489 (Fed. Cir. 1984). The skilled person readily appreciates that the phrase encompasses any unit from a plant from which progeny may be obtained. In light of all the foregoing, it is

clear that the metes and bounds of the phrase "reproductive unit" are clear to those skilled the relevant art.

In view of the forgoing remarks and the claim amendments, it is respectfully submitted that claims 2, 7, 11, 12, 18, and 21 as amended fully comply with the requirements set forth in 35 U.S.C. §112, second paragraph. Accordingly, withdrawal of the above-mentioned rejections is respectfully requested.

CLAIMS 1 AND 7 AS AMENDED ARE NOT ANTICIPATED BY CORUZZI ET AL.

The Examiner asserts that because Coruzzi et al. teach plant expression cassettes Z3 and Z17 comprising the pBIN vector with a 35S promoter operably linked to a pea glutamine synthetase (GS) cDNA having at least 70% sequence identity for both the protein and nucleic acid sequences provided in GenBank Accession number X69822, and a NOS terminator, this reference anticipates the subject matter of claims 1 and 7.

Applicants respectfully submit that claim 1 as amended is directed to plant expression cassettes comprising a GS coding sequence from gymnosperm. The GS used in the vectors of Coruzzi et al. is from pea, an angiosperm. Claim 7 has been amended to include a reference to SEQ ID NO: 3 which is isolated from gymnosperm. Inasmuch as Coruzzi et al. do not identically disclose each and every feature of the claims as amended, Applicants respectfully submit that the §102(e) rejection of claim 1 and 7 is improper and should be withdrawn.

AMENDED CLAIMS 1 AND 7-11 ARE NOT UNPATENTABLE OVER CORUZZI ET AL. IN VIEW OF CANTON ET AL. AND APPLICANT'S ADDMISSION

At page 7 of the Official Action, the Examiner states that "[i]t would have been *prima facie* obvious at the time of Applicant's invention to modify the expression cassette and *Agrobacterium* vector of Coruzzi to substitute the cDNA

encoding glutamine synthetase from *Pinus sylvestris* as taught by Canton for the nucleic acid from pea because the two nucleic acids are functionally equivalent in that they both encode glutamine synthetase". The Examiner further asserts that "[i]t would have been obvious to substitute one functional equivalent for another".

Applicants respectfully submit that the foregoing assertion is erroneous on its face.

It is well known in the art that GS from angiosperm and gymnosperm plants are biochemically and functionally distinct in their regulation and expression patterns. In angiosperm plants, e.g., pea, there are two major forms of GS: a cytosolic form expressed in roots and vascular tissues, such as GS1, and a plastid form expressed in photosynthetic tissues, such as GS2. In gymnosperm plants, e.g., pine, several GS1 genes have been characterized, but GS2, the plastid form observed in angiosperm plants, does not exist. Further GS1a from pine has features quite distinct from GS1 of angiosperm plants. For example, GS1a from pine is expressed in photosynthetic tissues and its expression is correlated with plastid development (Canovas et al., *Planta* 1991;185:372-378; Canton et al., *Plant Mol. Biol.* 1993;22:819-828; and Garcia-Gutierrez et al., *Plant J.* 1998;13:187-199). Neither of these features of pine GS1a is shared with other GS1 enzymes from angiosperm species, such as pea. Therefore, the GS enzymes from gymnosperm plants are not functionally equivalent to those from angiosperm plants, e.g., pea. Accordingly, claim 1 which is directed to a vector comprising a GS coding sequence from gymnosperm plants is not rendered obvious by the disclosure in Coruzzi et al., in view of Canton et al. and applicant's remarks.

Moreover, claim 7 has been amended to recite a glutamine synthetase coding sequence having the sequence of GenBank Sequence X69822, or a glutamine synthetase coding sequence

that is at least 70% identical to GenBank Sequence X69822, or a glutamine synthetase coding sequence that hybridizes to GenBank Sequence X69822 at moderate stringency. It is submitted that the pea GS coding sequence used in Coruzzi et al., GS1A (GenBank Accession No. M20663) and GS3A (GenBank Accession No. X04763) share only a 50.2% and a 61.9% similarity with GenBank Sequence X69822, respectively (See the nucleic acid sequence alignment attached hereto Exhibits A and B).

As mentioned above, the angiosperm or pea GS enzyme encoded by the vectors of Coruzzi et al. is NOT functionally equivalent to the gymnosperm or pine GS enzyme encoded by the sequences disclosed by Canton et al. It would, therefore, NOT have been obvious to substitute the pea GS coding sequence in the vectors of Coruzzi et al. with the pine GS coding sequence in Canton et al.

To establish a *prima facie* case of obviousness, three basic criteria must be met: (1) there must be some suggestion or motivation, either in the references themselves or in the knowledge generally available to one of ordinary skill in the art, to modify the reference or to combine reference teachings; (2) there must be a reasonable expectation of success; and (3) the prior art reference (or references when combined) must teach or suggest all the claimed limitations (MPEP §2143). In the instant case, because the GS coding sequences disclosed by Coruzzi et al. and by Canton et al. are NOT functionally equivalent, there would have been NO motivation for one of ordinary skill in the art to combine the two references and to replace the pea GS coding sequence in Coruzzi et al. with the pine GS coding sequence in Canton et al. Further, no success would have been expected by one of ordinary skilled to combine the disclosure of Coruzzi et al. and Canton et al. Accordingly, the Examiner has failed to establish a *prima facie* case of obviousness.

Moreover, in *in re Papesch*, 315 F.2d 381, 137 USPQ 43 (CCPA 1963) and *Ex parte Thumm*, 132 USPQ 66 (Bd. App. 1961), the court has established that the presence of a property not possessed by the prior art is evidence of nonobviousness. In the instant case, the claimed expression vectors comprise gymnosperm or pine GS coding sequences. These expression vectors possess properties not possessed by the expression vectors of Coruzzi et al., which comprise pea GS coding sequences. Specifically, as disclosed in the paragraphs begin at page 13, line 21, end at page 14, line 37 of the present application, when the instantly claimed vectors are transferred into angiosperm plants, the gymnosperm GS1 transcripts are correctly processed by the angiosperm translational machinery and the pine GS1 polypeptide is detectable both in leaf regions enriched in photosynthetic cells and in vascular elements. This unusual accumulation of the pine GS1 in photosynthetic tissues could not have been predicted from the normal accumulation of the endogenous angiosperm enzyme in vascular tissue only. Further, Coruzzi et al. have disclosed that when the expression vectors containing angiosperm GS coding sequences, GS3A or GS1A, are transferred into *Nicotiana tabacum* line SR1, only 6/13 or 5/8, respectively, of the transgenic plants demonstrate overexpression of GS activity (See column 26, lines 19-65 and column 27, lines 25-40 of Coruzzi). However, the transformation efficiency of the presently claimed vectors is unexpectedly higher, nearly 100%.

In summary, the requirements to establish a *prima facie* case of obviousness have not been met. Neither the cited references or the knowledge available to those skilled in the art teach or suggest any motivation to combine the teachings of Coruzzi et al. and Canton et al. Moreover, neither the references or the knowledge available to those skilled in the art provide any reasonable expectation of success in

substituting the pea GS coding sequences in the vectors of Coruzzi et al. with the pine GS coding sequences in Canton et al. Finally, the vectors of the present application possess unexpected properties over those disclosed in the prior art in that the present vectors possess higher transformation efficiency and that the transgenic plants containing the same have pine GS polypeptides present in photosynthetic cells. Accordingly, Applicants respectfully submit that the rejection of claims 1 and 7-11 under 35 U.S.C. §103(a) is untenable and should be withdrawn.

CONCLUSION

In view of the amendments and remarks presented herein, it is respectfully urged that the rejections set forth in the April 11, 2003 Official Action be withdrawn and that this application be passed to issue. In the event the Examiner is not persuaded as to the allowability of any claim, and it appears that any outstanding issues may be resolved through a telephone interview, the Examiner is requested to telephone the undersigned attorney at the phone number given below.

Respectfully submitted,

DANN, DORFMAN, HERRELL AND SKILLMAN
A Professional Corporation

By _____
Tong Li
PTO Registration No. 47,748

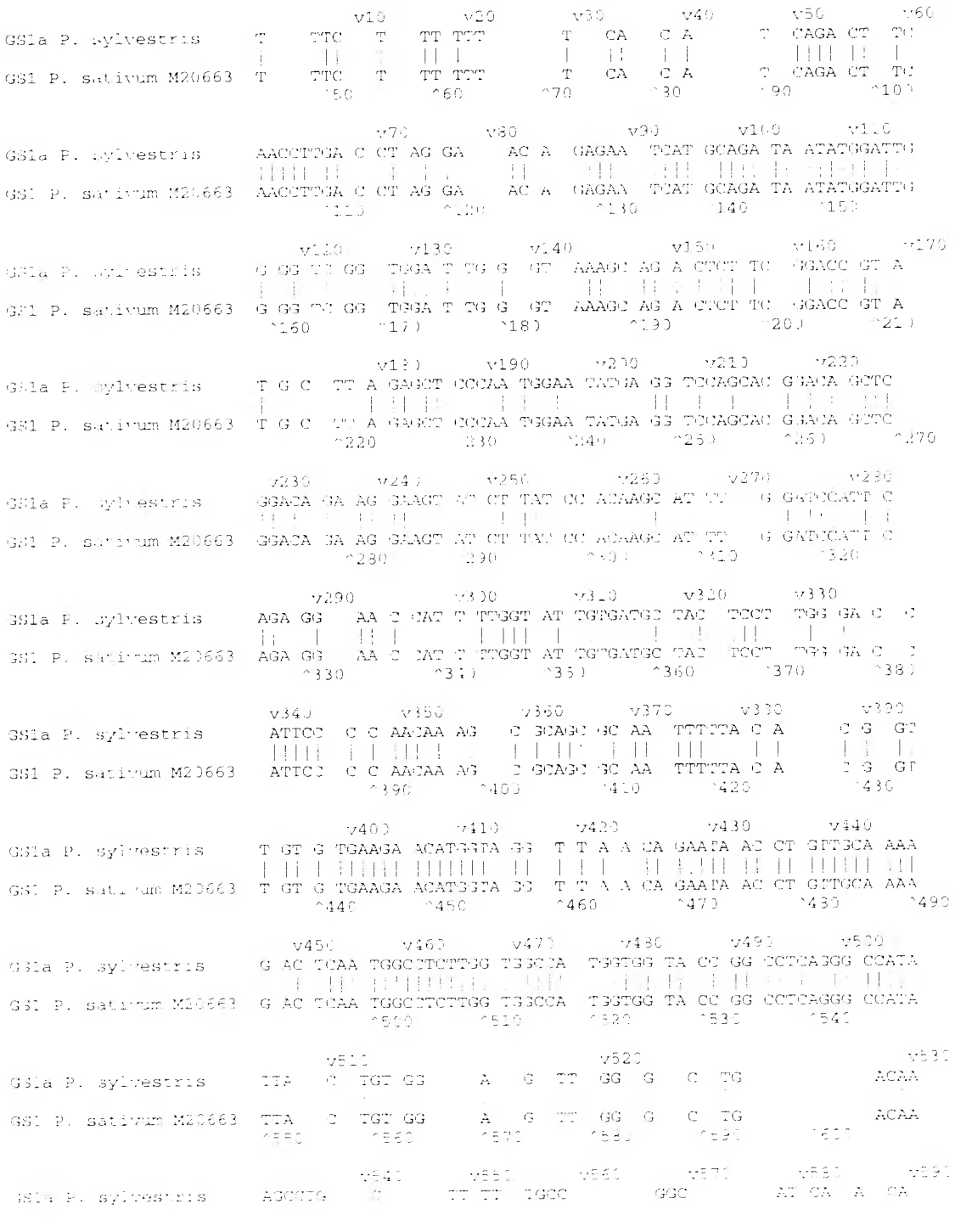
Telephone: (215) 563-4100
Facsimile: (215) 563-4044
Enclosures: Exhibits A and B and references describing INRA Clone

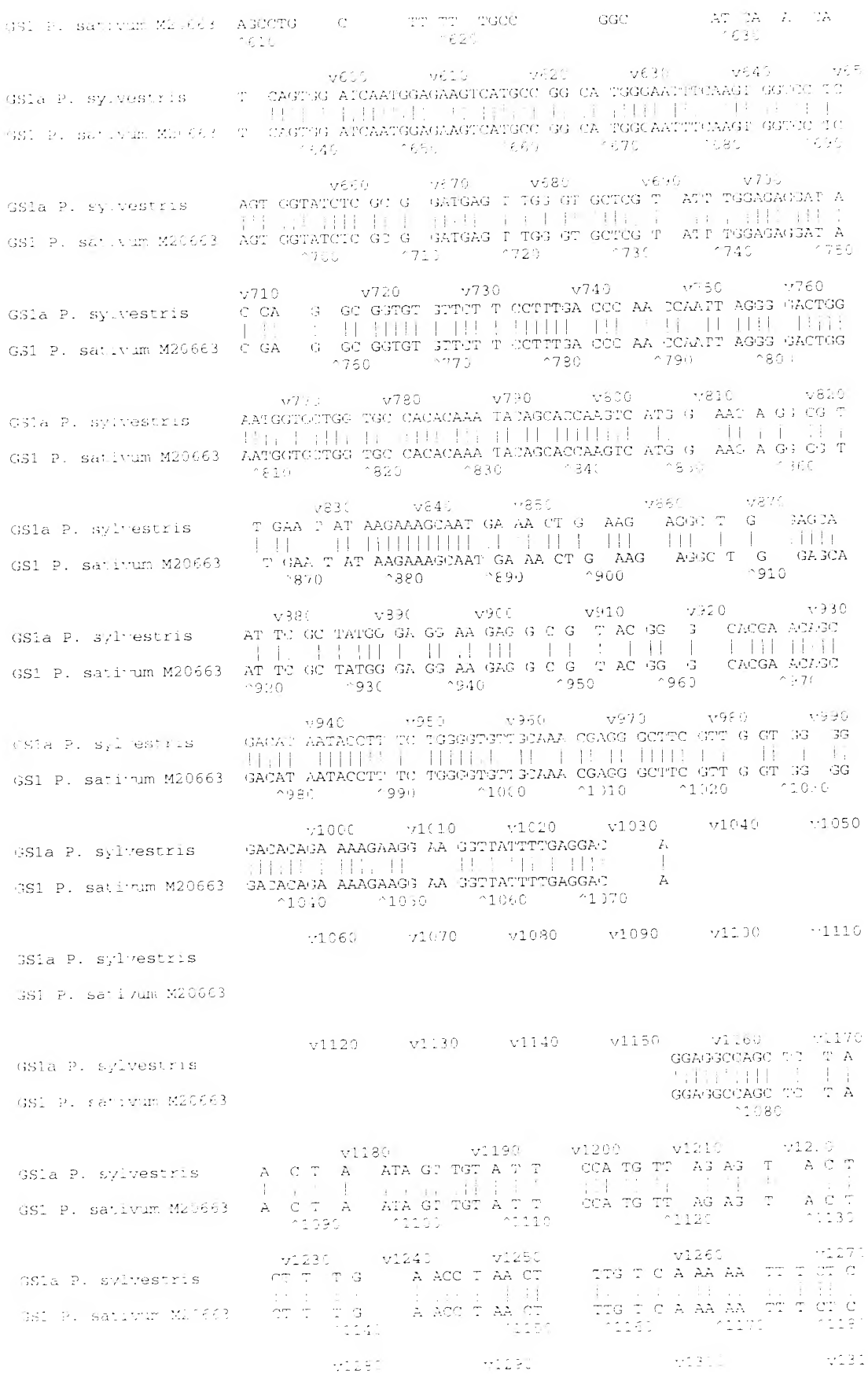
EXHIBIT A

DNA Alignment of GS1a from *P. sylvestris* (GenBank Accession No. 69822) with GS1A from *P. sativum* (GenBank Accession No. M20663)

Martinez/Needleman-Wunsch DNA Alignment
Minimum Match: 9; Gap Penalty: 1.10; Gap Length Penalty: 0.33

Seq1(1>1423) GS1a P. sylvestris	Seq2(1>1434) GS1 P. sativum M20663	Similarity Index	Gap Number	Gap Length	Consensus Length
(1>1423)	(44>1429)	50.2	177	481	1645





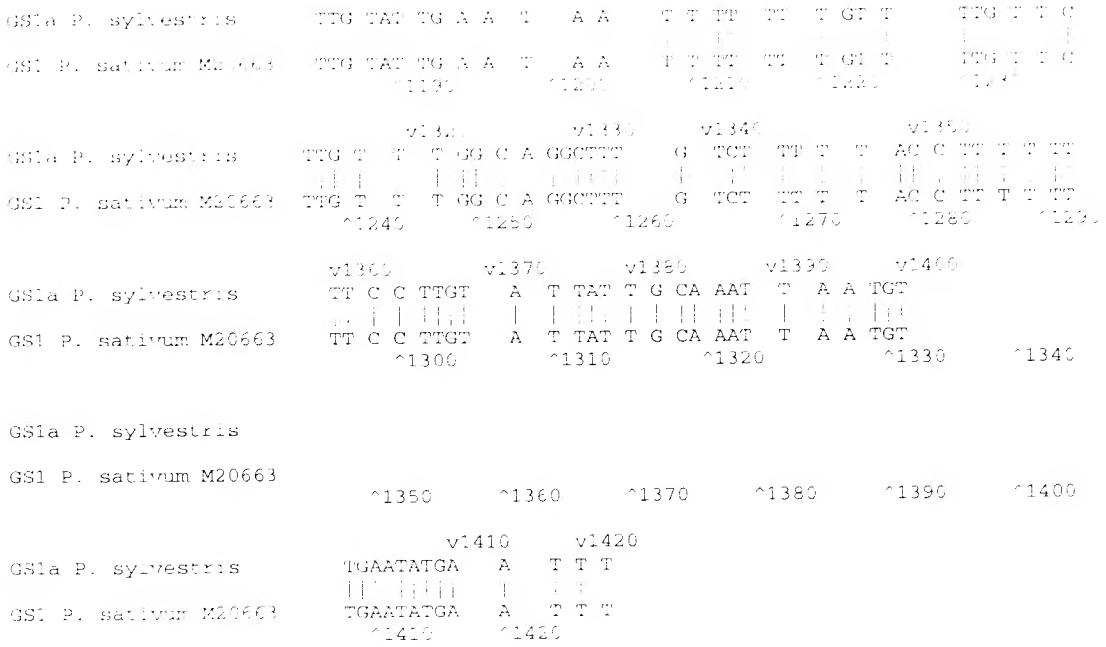

GS1a P. sylvestris
GS1 P. sativum M20663
^1240
^1250
^1260
^1270
^1280
^1290
^1300
^1310
^1320
^1330
^1340
^1350
^1360
^1370
^1380
^1390
^1400
^1410
^1420

EXHIBIT B

DNA Alignment of GS1a from *P. sylvestris* (GenBank Accession No. 69822) with GS3A from *P. sativum* (GenBank Accession No. X04763)

Martinez/Needleman-Wunsch DNA Alignment
Minimum Match: 9; Gap Penalty: 1.10; Gap Length Penalty: 0.33

Seq1(1>1423) GS1a P. sylvestris	Seq2(1>1373) X04763 GS3A P.sativum	Similarity Index	Gap Number	Gap Length	Consensus Length
(193>1293)	(219>1206)	61.9	96	217	1153
(1>1423)	(27>1336)	58.4	96	217	1475

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                 v10        v20        v30        v40        v50        v60
v70        v80        v90        v100
GS1a P. sylvestris
 T C T    T T   TT          T    CAT    G      A T   CAGA CT   TCAA   TT A CT     GA     ACAGA AAG T A
TTGC G
X04763 GS3A P.sativum"
 T C T    T T   TT          T    CAT    G      A T   CAGA CT   TCAA   TT A CT     GA     ACAGA AAG T A
TTGC G
                 ^30        ^40        ^50        ^60        ^70        ^80        ^90
^100       ^110       ^120

                 v110       v120       v130       v140       v150       v160
v170       v180       v190       v200
GS1a P. sylvestris
A TA ATATGG TTGG GGATCAGG AT GA AT  G AG AAAGCCAG  CTCT  C GGACC GTGAGT  C  T  A A CTTCC AA TG
GAACTA
X04763 GS3A P.sativum"
A TA ATATGG TTGG GGATCAGG AT GA AT  G AG AAAGCCAG  CTCT  C GGACC GTGAGT  C  T  A A CTTCC AA TG
GAACTA
                 ^130       ^140       ^150       ^160       ^170       ^180       ^190
^200       ^210       ^220

                 v210       v220       v230       v240       v250       v260
v270       v280       v290
GS1a P. sylvestris     TGA GG TC AGCAC   A
CA GC C AGGA A GA AG GAAGT ATT TATATCCACAAGCTAT TTC  G GA CCATT C G AGAGG AA A
X04763 GS3A P.sativum"  TGA GG TC AGCAC
A CA GC C AGGA A GA AG GAAGT ATT TATATCCACAAGCTAT TTC  G GA CCATT C G AGAGG AA A
                 ^230       ^240       ^250       ^260       ^270       ^280       ^290
^300       ^310       ^320

                 v300       v310       v320       v330       v340       v350
v360       v370       v380
GS1a P. sylvestris     A ATT TTG T AT TGTGATG  TAC C CC A  TGG GA C  C ATT CC  C CAA CAAGAG
C  TGC GC  C AAAATTTT A   AC
X04763 GS3A P.sativum"  A ATT TTG T AT TGTGATG  TAC C CC A  TGG GA C  C ATT CC
C CAA CAAGAG   C  TGC GC  C AAAATTTT A   AC
                 ^330       ^340       ^350       ^360       ^370       ^380
^390       ^400       ^410

                 v390       v400       v410       v420       v430       v440
v450       v460       v470
GS1a P. sylvestris     GA   G    TT G TG TGAAG  AC ATGGTA GG  TTGAACAAGA TATAC CT TT CA
AAAG AC TCAA TGGCC CT GG TGGCC AT
X04763 GS3A P.sativum"  GA   G    TT G TG TGAAG
AC ATGGTA GG  TTGAACAAGA TATAC CT TT CA AAAG AC TCAA TGGCC CT GG TGGCC AT
                 ^420       ^430       ^440       ^450       ^460       ^470
^480       ^490       ^500

                 v480       v490       v500       v510       v520       v530       v540
v550       v560       v570
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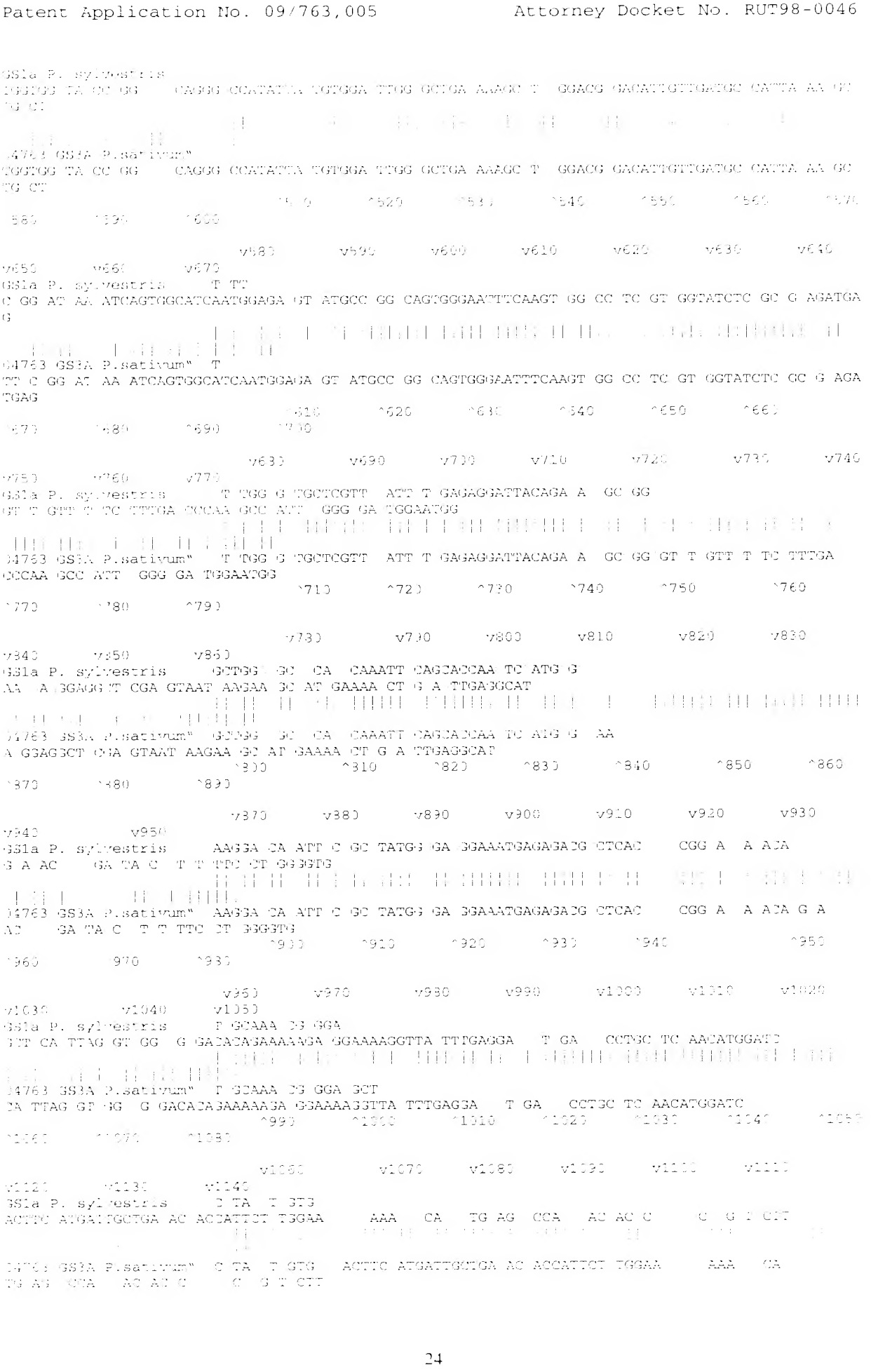

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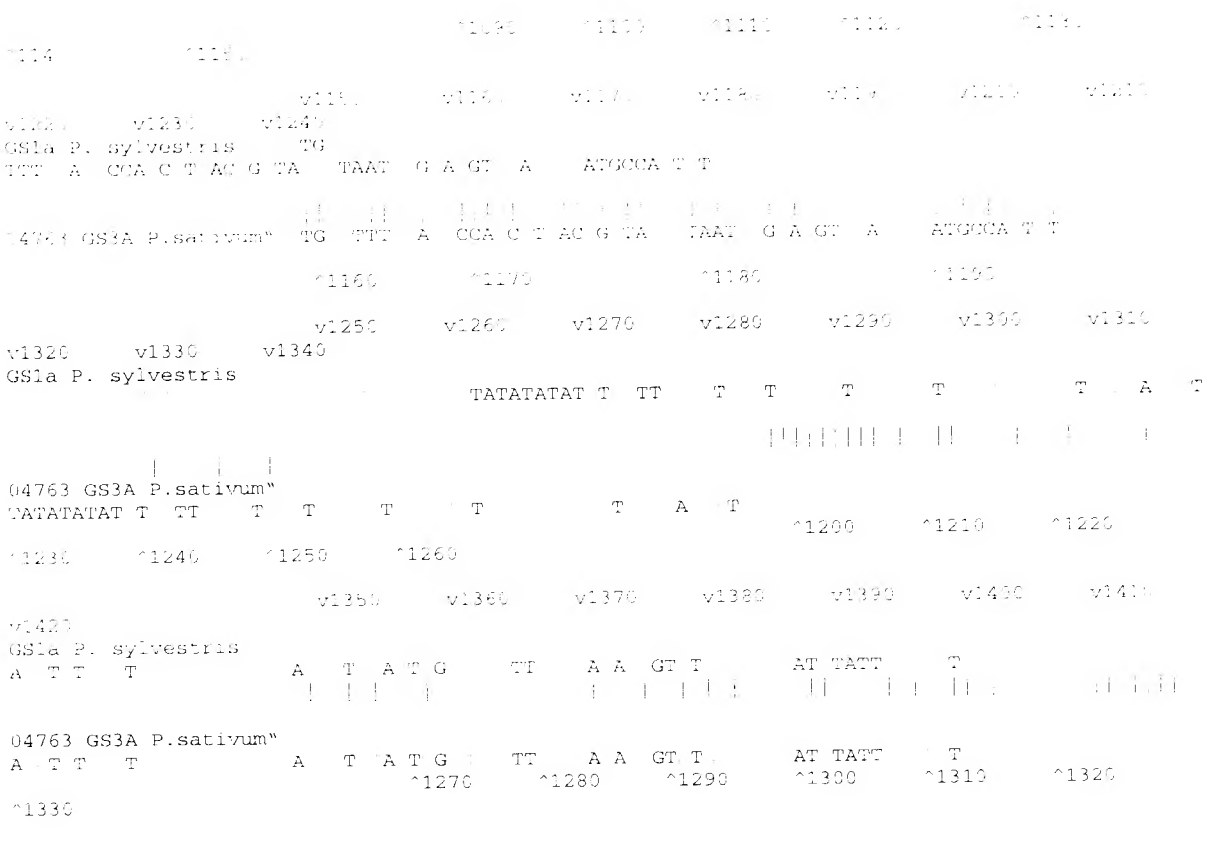
GS1a P. sylvestris
TTT A CCA C T AC G TA TAAT G A GT A ATGCCA T T
04763 GS3A P.sativum" TG TTT A CCA C T AC G TA TAAT G A GT A ATGCCA T T
GS1a P. sylvestris
TATATATAT T TT T T T T T A T
04763 GS3A P.sativum"
TATATATAT T TT T T T T T A T
GS1a P. sylvestris
A T T T A T G TT A A GT T AT TATT T
04763 GS3A P.sativum"
A T T T A T G TT A A GT T AT TATT T